

<110> Sharma, Satish Kumar Rank, Kenneth Bruce

 $<\!\!120\!\!>$ SOLUBLE NOTCH-BASED SUBSTRATES FOR GAMMA SECRETASE AND METHODS AND COMPOSITIONS FOR USING SAME

<130> PC27514A

<140> 10/717,244

<141> 2003-11-19

<160> 14

<170> PatentIn version 3.1

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<220> <223> DNA encoding synthetic fusion of notch and nus

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Asn Val Met Thr Val Asp Asp Leu Gln Ala Lys His Gln Ala Glu Ala 340 345 350 His Ala Ala Ile Asp Thr Phe Thr Lys Tyr Leu Asp Ile Asp Glu Asp 355 360 365 Phe Ala Thr Val Leu Val Glu Glu Gly Phe Ser Thr Leu Glu Glu Leu 370 380 Ala Tyr Val Pro Met Lys Glu Leu Leu Glu Ile Glu Gly Leu Asp Glu 385 390 395 400 Pro Thr Val Glu Ala Leu Arg Glu Arg Ala Lys Asn Ala Leu Ala Thr 405 410 415 Ile Ala Gln Ala Gln Glu Glu Ser Leu Gly Asp Asn Lys Pro Ala Asp 420 425 430 Asp Leu Leu Asn Leu Glu Gly Val Asp Arg Asp Leu Ala Phe Lys Leu 435 440 445 Ala Ala Arg Gly Val Cys Thr Leu Glu Asp Leu Ala Glu Gln Gly Ile 450 455 460 Asp Asp Leu Ala Asp Ile Glu Gly Leu Thr Asp Glu Lys Ala Gly Ala 465 470 475 480 Leu Ile Met Ala Ala Arg Asn Ile Cys Trp Phe Gly Asp Glu Ala Thr 485 490 495 Ser Gly Ser Gly His His His His His Ser Ala Gly Lys Glu Thr 500 510 Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser Pro Pro Pro Thr 515 520 525 Gly Leu Val Pro Arg Gly Ser Ala Gly Ser Gly Thr Ile Asp Asp Asp 530 540 Asp Lys Ser Pro Gly Ala Arg Gly Ser Glu Phe Asn Ile Pro Tyr Lys 545 550 555 560 Ile Glu Ala Val Lys Ser Glu Pro Val Glu Pro Pro Leu Pro Ser Gln
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Lys Asn Ala Ser Asp Gly Ala Leu Met Asp Asp Asn Gln Asn Glu Trp 645 650 655
Gly Asp Glu Asp Leu Glu Thr Lys Lys Phe Arg Phe Glu Glu Pro Val
660 665 670
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Gln His Leu Asp Ala Ala Asp Leu Arg Met Ser Ala Met Ala Pro Thr
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    Arg Gln His Gly Gln Leu Trp Phe Pro Glu Gly Phe Lys Val Ser 50 60
Glu Ala Ser Lys Lys Lys Arg Arg Glu Pro Leu Gly Glu Asp Ser Val 70 75 80
Gly Leu Lys Pro Leu Lys Asn Ala Ser Asp Gly Ala Leu Met Asp Asp
85 90 95
Asn Gln Asn Glu Trp Gly Asp Glu Asp Leu Glu Thr Lys Lys Phe Arg
100 105 110
Phe Glu Glu Pro Val Val Leu Pro Asp Leu Ser Asp Gln Thr Asp His
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Val Asp Gly Val Asn Thr Tyr Asn Cys Arg Cys Pro Pro Glu Val Thr 275 280 285 Gly Gln Tyr Cys Thr Glu Asp Val Asp Glu Cys Gln Leu Met Pro Asn 290 295 300 Ala Cys Gln Asn Ala Gly Thr Cys His Asn Thr His Gly Gly Tyr Asn 315 310 315Cys Val Cys Val Asn Gly Trp Thr Gly Glu Asp Cys Ser Glu Asn Ile 325 330 335 Asp Asp Cys Ala Ser Ala Ala Cys Phe Gln Gly Ala Thr Cys His Asp 340 345 350 Arg Val Ala Ser Phe Tyr Cys Glu Cys Pro His Gly Arg Thr Gly Leu 355 360 365 Leu Cys His Leu Lys His Ala Cys Ile Ser Asn Pro Cys Asn Glu Gly 370 380 Ser Asn Cys Asp Thr Asn Pro Val Asn Gly Lys Arg Ile Cys Thr Cys 385 390 395 400 Pro Ser Gly Tyr Thr Gly Pro Ala Cys Ser Gln Asp Val Asp Glu Cys 405 410 415 Asp Leu Gly Ala Asn Arg Cys Glu His Ala Gly Lys Cys Leu Asn Thr 420 425 430 Leu Gly Ser Phe Glu Cys Gln Cys Leu Gln Gly Tyr Thr Gly Pro Gly 435 440 445 Cys Glu Ile Asp Val Asn Glu Cys Ile Ser Asn Pro Cys Gln Asn Asp 450 455 460 Ala Thr Cys Leu Asp Gln Ile Gly Glu Phe Gln Cys Ile Cys Met Pro 465 470 475 480 Gly Tyr Glu Gly Val Tyr Cys Glu Ile Asn Thr Asp Glu Cys Ala Ser 485 490 495 Ser Pro Cys Leu His Asn Gly His Cys Met Asp Lys Ile His Glu Phe 500 510 Gln Cys Gln Cys Pro Lys Gly Phe Asn Gly His Leu Cys Gln Tyr Asp 515 520 525

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Leu Asn Gln Gly Thr Cys Ile Asp Asp Val Ala Gly Tyr Lys Cys Asn 805 810 815

Cys Pro Leu Pro Tyr Thr Gly Ala Thr Cys Glu Val Val Leu Ala Pro 820 825 830

Cys Ala Thr Ser Pro Cys Lys Asn Ser Gly Val Cys Lys Glu Ser Glu 835 840 845

Asp Tyr Glu Ser Phe Ser Cys Val Cys Pro Thr Gly Trp Gln Gly Gln 850 860

Thr Cys Glu Val Asp Ile Asn Glu Cys Val Lys Ser Pro Cys Arg His 865 870 875 880

Gly Ala Ser Cys Gln Asn Thr Asn Gly Ser Tyr Arg Cys Leu Cys Gln 885 890 895

Ala Gly Tyr Thr Gly Arg Asn Cys Glu Ser Asp Ile Asp Asp Cys Arg 900 905 910

Pro Asn Pro Cys His Asn Gly Gly Ser Cys Thr Asp Gly Ile Asn Thr 915 920 925

Ala Phe Cys Asp Cys Leu Pro Gly Phe Gln Gly Ala Phe Cys Glu Glu 930 940

Asp Ile Asn Glu Cys Ala Ser Asn Pro Cys Gln Asn Gly Ala Asn Cys 945 950 955 960

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Gly Ile His Cys Glu Asn Asn Thr Pro Asp Cys Thr Glu Ser Ser Cys 980 985 990

Phe Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Ser Phe Thr Cys Leu 995 1000 1005

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Ser Tyr Gly Thr Tyr Lys Cys Thr Cys Pro Gln Gly Tyr Thr Gly 1040 1050

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Val Ala Ser Asn Thr Ala Arg Gly Phe Ile Cys Arg Cys Pro Ala 1325 1330 1335

Gly Phe Glu Gly Ala Thr Cys Glu Asn Asp Ala Arg Thr Cys Gly 1340 1350

Ser Leu Arg Cys Leu Asn Gly Gly Thr Cys Ile Ser Gly Pro Arg 1355 1360 1365

Ser Pro Thr Cys Leu Cys Leu Gly Ser Phe Thr Gly Pro Glu Cys 1370 1375 1380

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Cys Leu Cys Pro Ala Lys Phe Asn Gly Leu Leu Cys His Ile Leu 1415 1420 1425

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- His Val Pro Glu Arg Leu Ala Ala Gly Thr Leu Val Leu Val Val 1565 1570
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- Gln Ser Ala Thr Asp Val Ala Ala Phe Leu Gly Ala Leu Ala Ser 1685 1690 1695
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Asp Asp Leu Gly Lys Ser Ala Leu His Trp Ala Ala Ala Val Asn 2015 2020 2025

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Asn Pro Leu Arg Pro Gly Val Thr Pro Gly Thr Leu Ser Thr Gln 2315 2320 2325

Ala Ala Gly Leu Gln His Ser Met Met Gly Pro Leu His Ser Ser 2330 2340

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Gln Glu Ser Gln Ala Leu Pro Thr Ser Leu Pro Ser Ser Met Val 2435 2440 2445

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Gly Gly Ala Phe Val Gly Pro Arg Cys Gln Asp Pro Asn Pro Cys Leu 50 60
Ser Thr Pro Cys Lys Asn Ala Gly Thr Cys His Val Val Asp Arg Arg 65 70 75 80
Gly Val Ala Asp Tyr Ala Cys Ser Cys Ala Leu Gly Phe Ser Gly Pro
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Leu Cys Leu Thr Pro Leu Asp Asn Ala Cys Leu Thr Asn Pro Cys Arg
Asn Gly Gly Thr Cys Asp Leu Leu Thr Leu Thr Glu Tyr Lys Cys Arg
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2520

2515

2510

135

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Pro Ser Gly Tyr Thr Gly Pro Ala Cys Ser Gln Asp Val Asp Glu Cys 405 410 415 Ser Leu Gly Ala Asn Pro Cys Glu His Ala Gly Lys Cys Ile Asn Thr 420 425 430 Leu Gly Ser Phe Glu Cys Gln Cys Leu Gln Gly Tyr Thr Gly Pro Arg 435 440 445 Cys Glu Ile Asp Val Asn Glu Cys Val Ser Asn Pro Cys Gln Asn Asp 450 455 460 Ala Thr Cys Leu Asp Gln Ile Gly Glu Phe Gln Cys Met Cys Met Pro 465 470 475 480 Gly Tyr Glu Gly Val His Cys Glu Val Asn Thr Asp Glu Cys Ala Ser 485 490 495 Ser Pro Cys Leu His Asn Gly Arg Cys Leu Asp Lys Ile Asn Glu Phe 500 505 510 Gln Cys Glu Cys Pro Thr Gly Phe Thr Gly His Leu Cys Gln Tyr Asp 515 520 525 Val Asp Glu Cys Ala Ser Thr Pro Cys Lys Asn Gly Ala Lys Cys Leu 530 540 Asp Gly Pro Asn Thr Tyr Thr Cys Val Cys Thr Glu Gly Tyr Thr Gly 545 550 555 Thr His Cys Glu Val Asp Ile Asp Glu Cys Asp Pro Asp Pro Cys His 565 570 575 Tyr Gly Ser Cys Lys Asp Gly Val Ala Thr Phe Thr Cys Leu Cys Arg 580 585 590 Pro Gly Tyr Thr Gly His His Cys Glu Thr Asn Ile Asn Glu Cys Ser 600 605Ser Gln Pro Cys Arg Leu Arg Gly Thr Cys Gln Asp Pro Asp Asn Ala 610 615 620 Tyr Leu Cys Phe Cys Leu Lys Gly Thr Thr Gly Pro Asn Cys Glu Ile 625 630 635 640 Asn Leu Asp Asp Cys Ala Ser Ser Pro Cys Asp Ser Gly Thr Cys Leu 645 650 655

Asp Lys Ile Asp Gly Tyr Glu Cys Ala Cys Glu Pro Gly Tyr Thr Gly 660 665 670 Ser Met Cys Asn Ser Asn Ile Asp Glu Cys Ala Gly Asn Pro Cys His 675 680 685 Asn Gly Gly Thr Cys Glu Asp Gly Ile Asn Gly Phe Thr Cys Arg Cys 690 700 Pro Glu Gly Tyr His Asp Pro Thr Cys Leu Ser Glu Val Asn Glu Cys 705 710 715 720 Asn Ser Asn Pro Cys Val His Gly Ala Cys Arg Asp Ser Leu Asn Gly 725 730 735 Tyr Lys Cys Asp Cys Asp Pro Gly Trp Ser Gly Thr Asn Cys Asp Ile 740 745 750 Asn Asn Glu Cys Glu Ser Asn Pro Cys Val Asn Gly Gly Thr Cys 755 760 765 Lys Asp Met Thr Ser Gly Ile Val Cys Thr Cys Arg Glu Gly Phe Ser 770 780 Gly Pro Asn Cys Gln Thr Asn Ile Asn Glu Cys Ala Ser Asn Pro Cys 785 790 795 800 Leu Asn Lys Gly Thr Cys Ile Asp Asp Val Ala Gly Tyr Lys Cys Asn 805 810 815 Cys Leu Leu Pro Tyr Thr Gly Ala Thr Cys Glu Val Val Leu Ala Pro 820 825 830 Cys Ala Pro Ser Pro Cys Arg Asn Gly Gly Glu Cys Arg Gln Ser Glu 835 840 845 Asp Tyr Glu Ser Phe Ser Cys Val Cys Pro Thr Ala Gly Ala Lys Gly 850 860 Gln Thr Cys Glu Val Asp Ile Asn Glu Cys Val Leu Ser Pro Cys Arg 865 870 875 His Gly Ala Ser Cys Gln Asn Thr His Gly Xaa Tyr Arg Cys His Cys 885 890 895 Gln Ala Gly Tyr Ser Gly Arg Asn Cys Glu Thr Asp Ile Asp Asp Cys 900 905 910

- Arg Pro Asn Pro Cys His Asn Gly Gly Ser Cys Thr Asp Gly Ile Asn 915 920 925
- Thr Ala Phe Cys Asp Cys Leu Pro Gly Phe Arg Gly Thr Phe Cys Glu 930 940
- Glu Asp Ile Asn Glu Cys Ala Ser Asp Pro Cys Arg Asn Gly Ala Asn 945 955 960
- Cys Thr Asp Cys Val Asp Ser Tyr Thr Cys Thr Cys Pro Ala Gly Phe 965 970 975
- Ser Gly Ile His Cys Glu Asn Asn Thr Pro Asp Cys Thr Glu Ser Ser 980 985 990
- Cys Phe Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Ser Phe Thr Cys 995 1000 1005
- Leu Cys Pro Pro Gly Phe Thr Gly Ser Tyr Cys Gln His Val Val 1010 1020
- Asn Glu Cys Asp Ser Arg Pro Cys Leu Leu Gly Gly Thr Cys Gln 1025 1030 1035
- Asp Gly Arg Gly Leu His Arg Cys Thr Cys Pro Gln Gly Tyr Thr 1040 1045 1050
- Gly Pro Asn Cys Gln Asn Leu Val His Trp Cys Asp Ser Ser Pro 1055 1060 1065
- Cys Lys Asn Gly Gly Lys Cys Trp Gln Thr His Thr Gln Tyr Arg 1070 1080
- Cys Glu Cys Pro Ser Gly Trp Thr Gly Leu Tyr Cys Asp Val Pro 1085 1090 1095
- Ser Val Ser Cys Glu Val Ala Ala Gln Arg Gln Gly Val Asp Val 1100 11105 1110
- Ala Arg Leu Cys Gln His Gly Gly Leu Cys Val Asp Ala Gly Asn 1115 1120 1125
- Thr His His Cys Arg Cys Gln Ala Gly Tyr Thr Gly Ser Tyr Cys 1130 1140
- Glu Asp Leu Val Asp Glu Cys Ser Pro Ser Pro Cys Gln Asn Gly 1145 1150 1155
- Ala Thr Cys Thr Asp Tyr Leu Gly Gly Tyr Ser Cys Lys Cys Val

Ala Gly Tyr His Gly Val Asn Cys Ser Glu Glu Ile Asp Glu Cys 1175 1180 1185

Leu Ser His Pro Cys Gln Asn Gly Gly Thr Cys Leu Asp Leu Pro 1190 1195 1200

Asn Thr Tyr Lys Cys Ser Cys Pro Arg Gly Thr Gln Gly Val His 1205 1210 1215

Cys Glu Ile Asn Val Asp Asp Cys Asn Pro Pro Val Asp Pro Val 1220 1230

Ser Arg Ser Pro Lys Cys Phe Asn Asn Gly Thr Cys Val Asp Gln 1235 1240 1245

Val Gly Gly Tyr Ser Cys Thr Cys Pro Pro Gly Phe Val Gly Glu 1250 1260

Arg Cys Glu Gly Asp Val Asn Glu Cys Leu Ser Asn Pro Cys Asp 1265 1270 1275

Ala Arg Gly Thr Gln Asn Cys Val Gln Arg Val Asn Asp Phe His 1280 1285 1290

Cys Glu Cys Arg Ala Gly His Thr Gly Arg Arg Cys Glu Ser Val 1295 1300 1305

Ala Val Ala Ser Asn Thr Ala Arg Gly Phe Ile Cys Lys Cys Pro 1325 1330 1335

Ala Gly Phe Glu Gly Ala Thr Cys Glu Asn Asp Ala Arg Thr Cys 1340 1350

Gly Ser Leu Arg Cys Leu Asn Gly Gly Thr Cys Ile Ser Gly Pro 1355 1360 1365

Arg Ser Pro Thr Cys Leu Cys Leu Gly Pro Phe Thr Gly Pro Glu 1370 1380

Cys Gln Phe Pro Ala Ser Ser Pro Cys Leu Gly Gly Asn Pro Cys 1385 1390 1395

Tyr Asn Gln Gly Thr Cys Glu Pro Thr Ser Glu Ser Pro Phe Tyr 1400 1410

Arg Cys Leu Cys Pro Ala Lys Phe Asn Gly Leu Leu Cys His Ile 1415 1420 1425 Leu Asp Tyr Ser Phe Gly Gly Gly Ala Gly Arg Asp Ile Pro Pro 1430 1440 Pro Leu Ile Glu Glu Ala Cys Glu Leu Pro Glu Cys Gln Glu Asp 1445 1450 1455 Ala Gly Asn Lys Val Cys Ser Leu Gln Cys Asn Asn His Ala Cys 1460 1470 Gly Trp Asp Gly Gly Asp Cys Ser Leu Asn Phe Asn Asp Pro Trp 1475 1480 1485 Lys Asn Cys Thr Gln Ser Leu Gln Cys Trp Lys Tyr Phe Ser Asp 1490 1495 1500 Gly His Cys Asp Ser Gln Cys Asn Ser Ala Gly Cys Leu Phe Asp 1505 1510 1515 Gly Phe Asp Cys Gln Arg Ala Glu Gly Gln Cys Asn Pro Leu Tyr 1520 1530 Asp Gln Tyr Cys Lys Asp His Phe Ser Asp Gly His Cys Asp Gln Gly Cys Asn Ser Ala Glu Cys Glu Trp Asp Gly Leu Asp Cys Ala 1550 1560 Glu His Val Pro Glu Arg Leu Ala Ala Gly Thr Leu Val Val Val 1565 1570 1575 Val Leu Met Pro Pro Glu Gln Leu Arg Asn Ser Ser Phe His Phe 1580 1585 1590 Leu Arg Glu Leu Ser Arg Val Leu His Thr Asn Val Val Phe Lys Arg Asp Ala His Gly Gln Gln Met Ile Phe Pro Tyr Tyr Gly Arg 1610 1615 1620 Glu Glu_Glu Leu Arg Lys His_Pro Ile Lys Arg Ala_Ala Glu Gly Trp Ala Ala Pro Asp Ala Leu Leu Gly Gln Val Lys Ala Ser Leu 1640 1645 1650

- Leu Pro Gly Gly Ser Glu Gly Gly Arg Arg Arg Glu Leu Asp 1655 1660 1665
- Pro Met Asp Val Arg Gly Ser Ile Val Tyr Leu Glu Ile Asp Asn 1670 1680
- Arg Gln Cys Val Gln Ala Ser Ser Gln Cys Phe Gln Ser Ala Thr 1685 1690
- Asp Val Ala Ala Phe Leu Gly Ala Leu Ala Ser Leu Gly Ser Leu 1700 1710
- Asn Ile Pro Tyr Lys Ile Glu Ala Val Gln Ser Glu Thr Val Glu 1715 1720 1725
- Pro Pro Pro Ala Gln Leu His Phe Met Tyr Val Ala Ala Ala 1730 1740
- Ala Phe Val Leu Leu Phe Phe Val Gly Cys Gly Val Leu Leu Ser 1745 1750
- Arg Lys Arg Arg Xaa Gln His Gly Gln Leu Trp Phe Pro Glu Gly 1760 1770
- Phe Lys Val Ser Glu Ala Ser Lys Lys Lys Arg Arg Glu Xaa Leu 1775 1780 1785
- Gly Glu Asp Ser Val Gly Leu Lys Pro Leu Lys Asn Ala Ser Asp
- Gly Ala Leu Met Asp Asp Asn Gln Asn Glu Trp Gly Asp Glu Asp 1805 1810 1815
- Leu Glu Thr Lys Lys Phe Arg Phe Glu Glu Pro Val Val Leu Pro 1820 1830
- Asp Leu Asp Asp Gln Thr Asp His Arg Gln Trp Thr Gln Gln His 1835 1840 1845
- Leu Asp Ala Ala Asp Leu Arg Met Ser Ala Met Ala Pro Thr Pro 1850 1860
- Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val Asn Val Arg 1865 1870 1875
- Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser Cys Ser Gly 1880 1890

Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu Glu Asp Ala Pro 1895 1900 1905 Ala Val Ile Ser Asp Phe Ile Tyr Gln Gly Ala Ser Leu His Asn Gln Thr Asp Arg Thr Gly Glu Thr Ala Leu His Leu Ala Ala Arg 1930 Tyr Ser Arg Ser Asp Ala Ala Lys Arg Leu Leu Glu Ala Ser Ala Asp Ala Asn Ile Gln Asp Asn Met Gly Arg Thr Pro Leu His Ala Ala Val Ser Ala Asp Ala Gln Gly Val Phe Gln Ile Leu Ile Arg Asn Arg Ala Thr Asp Leu Asp Ala Arg Met His Asp Gly Thr Thr 1985 1990 1995 Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu Gly Met Leu Glu 2000 2010 Asp Leu Ile Asn Ser His Ala Asp Val Asn Ala Val Asp Asp Leu 2015 2020 2025 Gly Lys Ser Ala Leu His Trp Ala Ala Ala Val Asn Asn Val Asp 2030 2040 2040 Ala Ala Val Val Leu Leu Lys Asn Gly Ala Asn Lys Asp Met Gln 2045 2055 Asn Asn Arg Glu Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly 2060 2070 Ser Tyr Glu Thr Ala Lys Val Leu Leu Asp His Phe Ala Asn Arg 2075 2080 2085 Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Ile Ala Gln 2090 2100 Glu Arg Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr Asn 2105 2110 2115 Leu Val Arg Ser Pro Gln Leu His Gly Ala Pro Leu Gly Gly Thr

Pro Thr Leu Ser Pro Pro Leu Cys Ser Pro Asn Gly Tyr Leu Gly

Ser Leu Lys Pro Gly Val Gln Gly Lys Lys Val Arg Lys Pro Ser Ser Lys Gly Leu Ala Cys Gly Ser Lys Glu Ala Lys Asp Leu Lys 2165 2170 2175 Ala Arg Arg Lys Lys Ser Gln Asp Gly Lys Gly Cys Leu Leu Asp 2180 2185 2190 Ser Ser Gly Met Leu Ser Pro Val Asp Ser Leu Glu Ser Pro His 2195 2200 2205 Gly Tyr Leu Ser Asp Val Ala Ser Pro Pro Leu Leu Pro Ser Pro 2220 Phe Gln Gln Ser Pro Ser Val Pro Leu Asn His Leu Pro Gly Met 2225 2230 2235 Pro Asp Thr His Leu Gly Ile Gly His Leu Asn Val Ala Ala Lys 2240 2245 2250 Pro Glu Met Ala Ala Leu Gly Gly Gly Gly Arg Leu Ala Phe Glu 2255 2260 2265 Thr Gly Pro Pro Arg Leu Ser His Leu Pro Val Ala Ser Gly Thr Ser Thr Val Leu Gly Ser Ser Ser Gly Gly Ala Leu Asn Phe Thr 2285 2290 2295 Val Gly Gly Ser Thr Ser Leu Asn Gly Gln Cys Glu Trp Leu Ser Arg Leu Gln Ser Gly Met Val Pro Asn Gln Tyr Asn Pro Leu Arg 2315 Gly Ser Val Ala Pro Gly Pro Leu Ser Thr Gln Ala Pro Ser Leu 2330 Gln His Gly Met Val Gly Pro Leu His Ser Ser Leu Ala Ala Ser 2345 Ala Leu Ser Gln Met Met Ser Tyr Gln Gly Leu Pro Ser Thr Arg 2360 Leu Ala Thr Gln Pro His Leu Val Gln Thr Gln Gln Val Gln Pro 2375 2380 2385

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Phe Leu Ser Gly Glu Pro Ser Gln Ala Asp Val
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       Amino acid sequence surrounding the transmembrane domains of APP
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Ala Thr Val Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys 20 25 30
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      Artificial sequence
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Leu Ile Leu Ala Val Cys Ile Ala Val Asn Ser Arg Arg 20 25 30
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       Artificial sequence
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       Sequence surrounding the transmembrane domains of Notch-1
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Gln Asn Leu Gln Met Gln Gln Gln Asn Leu Gln Pro Ala Asn Ile

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<213> Artificial sequence

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<223> Sequence surrounding the transmembrane domains of Notch-1

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Pro Leu Pro Ser Gln Leu His Leu Met Tyr Val Ala Ala Ala Ala Phe 20 25 30

Val Leu Leu Phe Phe Val Gly Cys Gly Val Leu Leu Ser Arg Lys Arg 35 40 45

Arg Arg Gln His Gly Gln Leu Trp Phe Pro Glu Gly Phe Lys Val Ser 50 60

Glu Ala Ser Lys Lys Lys Arg Arg Glu Pro Leu Gly Glu Asp Ser Val 65 70 75 80

Gly Leu Lys Pro Leu Lys Asn Ala Ser Asp Gly Ala Leu Met Asp Asp 85 90 95

Asn Gln Asn Glu Trp Gly Asp Glu Asp Leu Glu Thr Lys Lys Phe Arg 100 105 110

Phe Glu Glu Pro Val Val Leu Pro Asp Leu Ser Asp Gln Thr Asp His 115 120 125

Arg Gln Trp Thr Gln Gln His Leu Asp Ala Ala Asp Leu Arg Met Ser 130 135 140

Ala Met Ala Pro Thr Pro Pro Gln Gly Glu Val Asp Ala Asp

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<211> 8

<212> PRT

Artificial sequence <213>

<220>

C-terminal flag sequence

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Asp Tyr Lys Asp Asp Asp Lys

1

5
       12
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       16
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<220>
<223> Flag/8 his tag
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Asp Tyr Lys Asp Asp Asp Asp Lys His His His His His His 10 15
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       1665
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       Nucleic acid encoding NusA
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                                                                      120
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caagagatcg acgtccgcgt acagatcgat cgcaaaagcg gtgattttga cactttccgt
                                                                      180
cgctggttag ttgttgatga agtcacccag ccgaccaagg aaatcaccct tgaagccgca
                                                                      240
Cgttatgaag atgaaagcct gaacctgggc gattacgttg aagatcagat tgagtctgtt
                                                                      300
acctttgacc gtatcactac ccagacggca aaacaggtta tcgtgcagaa agtgcgtgaa
                                                                      360
                                                                      420
gccgaacgtg cgatggtggt tgatcagttc cgtgaacacg aaggtgaaat catcaccggc
                                                                      480
gtggtgaaaa aagtaaaccg cgacaacatc tctctggatc tgggcaacaa cgctgaagcc
                                                                      540
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ggcgtgctct attccgttcg cccggaagcg cgtggcgcgc aactgttcgt cactcgttcc
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                                                                      660
                                                                      720
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gCggtgtcta ctgaactggg tggcgagcgt atcgatatcg tcctgtggga tgataacccg
                                                                      840
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aacggtcaga acgtgcgtct ggcttcgcaa ctgagcggtt gggaactcaa cgtgatgacc
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catcaccatc accatcactc cgcgggtaaa ga	gaaaccgctg	ctgcgaaatt	tgaacgccag	1560
cacatggact cgccaccgcc aactggtctg g	tcccccggg	gcagcgcggg	ttctggtacg	1620
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<220>

<223> Protein sequence encoding NusA

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Met Asn Lys Glu Ile Leu Ala Val Val Glu Ala Val Ser Asn Glu Lys 1 10 15

Ala Leu Pro Arg Glu Lys Ile Phe Glu Ala Leu Glu Ser Ala Leu Ala 20 25 30

Thr Ala Thr Lys Lys Lys Tyr Glu Gln Glu Ile Asp Val Arg Val Gln 35 40 45

Ile Asp Arg Lys Ser Gly Asp Phe Asp Thr Phe Arg Arg Trp Leu Val 50 60

Val Asp Glu Val Thr Gln Pro Thr Lys Glu Ile Thr Leu Glu Ala Ala 65 70 75 80

Arg Tyr Glu Asp Glu Ser Leu Asn Leu Gly Asp Tyr Val Glu Asp Gln 85 90 95

Ile Glu Ser Val Thr Phe Asp Arg Ile Thr Thr Gln Thr Ala Lys Gln 100 105 110

Val Ile Val Gln Lys Val Arg Glu Ala Glu Arg Ala Met Val Val Asp 115 120 125

Gln Phe Arg Glu His Glu Gly Glu Ile Ile Thr Gly Val Val Lys Lys

<211> 555

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<213> Artificial sequence

140

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Pro Thr Val Glu Ala Leu Arg Glu Arg Ala Lys Asn Ala Leu Ala Thr 405 410 415

Ile Ala Gln Ala Gln Glu Glu Ser Leu Gly Asp Asn Lys Pro Ala Asp 420 425 430

Asp Leu Leu Asn Leu Glu Gly Val Asp Arg Asp Leu Ala Phe Lys Leu 435 440 445

Ala Ala Arg Gly Val Cys Thr Leu Glu Asp Leu Ala Glu Gln Gly Ile 450 455 460

Asp Asp Leu Ala Asp Ile Glu Gly Leu Thr Asp Glu Lys Ala Gly Ala 465 470 475 480

Leu Ile Met Ala Ala Arg Asn Ile Cys Trp Phe Gly Asp Glu Ala Thr 485 490 495

Ser Gly Ser Gly His His His His His Ser Ala Gly Lys Glu Thr 500 505 510

Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser Pro Pro Pro Thr 515 520 525

Gly Leu Val Pro Arg Gly Ser Ala Gly Ser Gly Thr Ile Asp Asp Asp 530 540

Asp Lys Ser Pro Gly Ala Arg Gly Ser Glu Phe 545 550 555